

Sequence No. : 1

Sequence type: Nucleic acid

Topology: Linear

Sequence description

GGA AAG CTC CCT TTC TCA AGA ATG CCC ATC TGT GAA CAC ATG GTA GAG 48

| | | | |
|---|---|----|----|
| 1 | 5 | 10 | 15 |
|---|---|----|----|

15 Ser Pro Thr Cys Ser Gln Met Ser Asn Leu Val Cys Gly Thr Asp Gly

CTC ACA TAT ACG AAT GAA TGC CAG CTC TGC TTG GCC CGG ATA AAA ACC 144

35 40 45

Lys Gln Asp Ile Gln Ile Met Lys Asp Gly Lys Cys

50 55 60

Sequence length: 398

Strandedness: Double

30 Sequence kind: cDNA to mRNA

Animal name: Homo sapiens

Cell kind: Stomach cancer tissue

Clone name: HP00839

Characterization code: CDS

Existence position: 43..303

Sequence description

40 GCAGGCCCCA GCCAGCTCAG GCTACACTAT CCCAGGATCA GC ATG GCC GTC CGC 54

| | | | | | | | | | | | | | | | Met | Ala | Val | Arg | | | | |
|----|------------|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | | | | | | | | | | | | | | | 1 | | | | | | | |
| | CAG | TGG | GTA | ATC | GCC | CTG | GCC | TTG | GCT | GCC | CTC | CTT | GTT | GTG | GAC | AGG | 102 | | | | | |
| | Gln | Trp | Val | Ile | Ala | Leu | Ala | Leu | Ala | Ala | Leu | Leu | Val | Val | Asp | Arg | | | | | | |
| 5 | 5 | 10 | | | | | 15 | | | | | 20 | | | | | | | | | | |
| | GAA | GTG | CCA | GTG | GCA | GCA | GGA | AAG | CTC | CCT | TTC | TCA | AGA | ATG | CCC | ATC | 150 | | | | | |
| | Glu | Val | Pro | Val | Ala | Ala | Gly | Lys | Leu | Pro | Phe | Ser | Arg | Met | Pro | Ile | | | | | | |
| | 25 | | | | | 30 | | | | | 35 | | | | | | | | | | | |
| | TGT | GAA | CAC | ATG | GTA | GAG | TCT | CCA | ACC | TGT | TCC | CAG | ATG | TCC | AAC | CTG | 198 | | | | | |
| 10 | Cys | Glu | His | Met | Val | Glu | Ser | Pro | Thr | Cys | Ser | Gln | Met | Ser | Asn | Leu | | | | | | |
| | 40 | | | | | 45 | | | | | 50 | | | | | | | | | | | |
| | GTC | TGC | GGC | ACT | GAT | GGG | CTC | ACA | TAT | ACG | AAT | GAA | TGC | CAG | CTC | TGC | 246 | | | | | |
| | Val | Cys | Gly | Thr | Asp | Gly | Leu | Thr | Tyr | Thr | Asn | Glu | Cys | Gln | Leu | Cys | | | | | | |
| | 55 | | | | | 60 | | | | | 65 | | | | | | | | | | | |
| 15 | TTG | GCC | CGG | ATA | AAA | ACC | AAA | CAG | GAC | ATC | CAG | ATC | ATG | AAA | GAT | GGC | 294 | | | | | |
| | Leu | Ala | Arg | Ile | Lys | Thr | Lys | Gln | Asp | Ile | Gln | Ile | Met | Lys | Asp | Gly | | | | | | |
| | 70 | | | | | 75 | | | | | 80 | | | | | | | | | | | |
| | AAA | TGC | TGATCCCACA | GGAGCACCTC | AAGCCATGAA | GTGTCAGCTG | GAGAACAGTG | 350 | | | | | | | | | | | | | | |
| | Lys | Cys | | | | | | | | | | | | | | | | | | | | |
| 20 | 85 | | | | | | | | | | | | | | | | | | | | | |
| | GTGGGCATGG | AGAGGATATG | ACATGAAATA | AAAGATCCAG | CCCAACTG | 398 | | | | | | | | | | | | | | | | |